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Sequence logo showing the conservation of amino acids across 10 homologous proteins. The x-axis shows positions 1 to 34. The y-axis lists amino acids: * (stop), G, C, T, A, D, S, E, P, R, Y, F, I, V, M, L, W, H, N, K, Q, B, Z, X. Conservation is indicated by color: green (high), yellow (moderate), red (low). Stop codons are marked with an asterisk (*).

ir ybjE_TRIP1a

p35 5.5 bits

{-----} sd-(12)-ir 914208 Gap 4.0 bits

|-----| sd-ir 914208 ybjE_TRIP1a- total 9.5 bits

p10 3.7 bit

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{-----} p35-(25)-p10 914211 Gap 4.0 bit  
{-----} p35-p10 914211 total 5.2 bits
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* * 914150 * * 914140 * * 914130 * * 914141

The figure displays a protein sequence alignment across eight positions (914180, 914170, 914160, 914150, 914140, 914130, 914120, 914110). The top row shows the amino acid sequence with mutations highlighted by red dots. The bottom row shows the corresponding codons. Positions 914180, 914170, 914160, 914150, 914140, 914130, and 914120 each have a red dot above the sequence, indicating a mutation at that position. Position 914110 has a red dot above the codon, indicating a mutation at that position.

[####> orf 16 codons p35 5.7 bits

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} p35-(23)-p10 914129 Gap 1.4 bits
p35-p10 914129 total 7.0 bits

10

p10 2.1 bits

{-----} p35-(22)-p10 914076 Gap 2.3 bits
----- p35-p10 914076 total 5.8 bits

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